Transcriptional profiling of feline infectious peritonitis virus infection in CRFK cells and in PBMCs from FIP diagnosed cats

ABSTRACT

Feline Infectious Peritonitis (FIP) is a lethal systemic disease, caused by the FIP Virus (FIPV); a virulent mutant of Feline Enteric Coronavirus (FECV). Currently, the viruses virulence determinants and host gene expressions during FIPV infection are not fully understood. RNA sequencing of Crandell Rees Feline Kidney (CRFK) cells, infected with FIPV strain 79–1146 at 3 hours post infection (h.p.i), were sequenced using the Illumina next generation sequencing approach. Bioinformatic's analysis, based on Felis catus 2X annotated shotgun reference genome, using CLC bio Genome Workbench mapped both control and infected cell reads to 18899 genes out of 19046 annotated genes. Kal's Z test statistical analysis was used to analyse the differentially expressed genes from the infected CRFK cells. Real time RT-qPCR was developed for further transcriptional profiling of three genes (PD-1, PD-L1 and A3H) in infected CRFK cells and Peripheral Blood Mononuclear Cells (PBMCs) from healthy and FIP-diseased cats.

Keyword: FIPV; CRFK; PBMCs; Transcriptome; RT-qPCR; Gene expression; Fold change